

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/601,777A
Source: 1FW16
Date Processed by STIC: 11/28/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER: 10/601,777A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. **Do not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
 Sequence(s) 5 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/601,777A

DATE: 11/28/2005

TIME: 11:00:12

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\11282005\J601777A.raw

2 <110> APPLICANT: Okamoto, Tadashi
 3 Takase, Hiromitsu
 4 Hashimoto, Hiroyuki

W--> 5 <120> TITLE OF INVENTION: A METHOD FOR ACQUIRING INFORMATION OF A BIOCHIP USING TIME OF FLIGHT

W--> 6 SECONDARY ION MASS SPECTROMETRY AND AN APPARATUS FOR ACQUIRING INFORMATION FOR
 W--> 7 THE APPLICATION THEREOF

W--> 8 <130> FILE REFERENCE: 03560.003310

W--> 9 <140> CURRENT APPLICATION NUMBER: US/10/601,777A

10 <141> CURRENT FILING DATE: 2003-06-24

11 <150> PRIOR APPLICATION NUMBER: JP 2002-191208

12 <151> PRIOR FILING DATE: 2002-06-28

13 <150> PRIOR APPLICATION NUMBER: JP 2003-161862

14 <151> PRIOR FILING DATE: 2003-06-06

W--> 15 <160> NUMBER OF SEQ ID: 5

W--> 16 <210> SEQ ID NO: 1

17 <211> LENGTH: 40

18 <212> TYPE: DNA

19 <213> ORGANISM: Artificial sequence

W--> 20 <220> FEATURE:

21 <223> OTHER INFORMATION: Sample oligonucleotide

R.J.

W--> 22 <400> SEQUENCE: 1

23 tttttttttt tttttttttt tttttttttt 40

24 <210> SEQ ID NO: 2

25 <211> LENGTH: 50

26 <212> TYPE: DNA

27 <213> ORGANISM: Artificial sequence

W--> 28 <220> FEATURE:

29 <223> OTHER INFORMATION: Sample oligonucleotide

W--> 30 <400> SEQUENCE: 2

31 tgccaggcatg caagctggc actggccgtc gttttacaac gtcgtgactg 50

32 <210> SEQ ID NO: 3

33 <211> LENGTH: 20

34 <212> TYPE: RNA

35 <213> ORGANISM: Artificial sequence

W--> 36 <220> FEATURE:

37 <223> OTHER INFORMATION: Sample oligonucleotide

W--> 38 <400> SEQUENCE: 3

39 uuuuuuuuuuu uuuuuuuuuuu 20

40 <210> SEQ ID NO: 4

41 <211> LENGTH: 18

42 <212> TYPE: DNA

43 <213> ORGANISM: Artificial sequence

W--> 44 <220> FEATURE:

*Dose Not Comply
Connected Diskette Neede*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/601,777A

DATE: 11/28/2005
TIME: 11:00:12

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11282005\J601777A.raw

45 <223> OTHER INFORMATION: Sample oligonucleotide
W--> 46 <400> SEQUENCE: 4
47 actggccgtc gtttaca 18
48 <210> SEQ ID NO: 5
49 <211> LENGTH: 50
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial sequence
W--> 52 <220> FEATURE:
53 <221> NAME/KEY: misc_feature
54 <222> LOCATION: (1)..(1)
55 <223> OTHER INFORMATION: n is NCys-NH- (CH₂)₂-O- (CH₂)₂-O-CH₂CONH-T
W--> 56 <400> SEQUENCE: 5
W--> 57 ngcaggcatg caagcttggc actggccgtc gtttacaac gtcgtgactg 50

Needs explanation in <220>-<223>
section

(see item 11
on Error
summary
sheet)

(your previous
submission
showed

<220>
<223> Sample oligonucleotide

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/28/2005
PATENT APPLICATION: US/10/601,777A TIME: 11:00:13

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11282005\J601777A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 1

VERIFICATION SUMMARY

DATE: 11/28/2005

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TIME: 11:00:13

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\11282005\J601777A.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:16 M:283 W: Missing Blank Line separator, <210> field identifier
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:30 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0